REMARKS

Upon entry of the present amendments, claims 5, 10-15, 25, and 26 will be pending. Claims 8, 9, 23 and 24 have been canceled herein without prejudice or disclaimer. Claims 5, 7, 10, 11, 25, and 26 have been amended. The amendments are supported by the specification and original claims and, therefore, do not add new matter.

Rejection Under 35 U.S.C. § 102(b)

The rejection of claims 8 and 11-15 under 35 U.S.C. 102(b), as allegedly being anticipated by Goodearl et al. (June 1999) WO 99/28470, is respectfully traversed.

It is alleged that claims 8 and 11-15 are anticipated by Goodearl because the claims require only that the polynucleotide comprise at least 15 bases of and is capable of specifically hybridizing under highly stringent conditions to the nucleic acids fo the Markush group and that the polynucleotide of Goodearl meets these limitations. Applicants respectfully traverse. While the Applicants maintain the traversal previously made of record and submit that Goodearl fails to disclose any 15 nucleotide sequences, the claims have been amended and are no longer drawn to a polynucleotide containing only 15 continuous bases, although Applicants expressly reserve the right to pursue this subject matter in a related application. In particular, claim 8 has been canceled and claim 11 has been amended to depend from claim 7. As such, the current amendments render the rejection moot.

Accordingly, for the reasons set forth above, withdrawal of the rejection of claims 8 and 11-15 under 35 U.S.C. § 102(b), as being anticipated by Goodearl et al. is respectfully requested.

Rejection Under 35 U.S.C. § 112

Applicants respectfully traverse the rejection of claims 5, 7-15, and 23-26 under 35 U.S.C. 112, first paragraph, as allegedly failing to comply with the written description requirement.

It is alleged in the Office action that the claimed polynucleotide sequences are defined in the claims using an indefinite article and, therefore, the structural limitations set forth in the claims would be present in many functionally divergent molecules. In particular, the polynucleotides of claims 7-15 and 23-26 are interpreted by the Examiner as broadly encompasing any nucleic acid encoding "a polypeptide having an amino acid sequence" or "having a nucleotide sequence" that can include any sequence set forth in the identified SEQ ID NO, including fragments of the identified SEQ ID NO's of two or more amino acids/nucleotides in length. For example, with respect to claims 5 and 7, the Examiner has interpreted the phrase "having an amino acid sequence as set forth in SEQ ID NO:2" as broadly including any amino acid sequence set forth in SEQ ID NO:2, including any two or more amino acid sequence fragment of SEQ ID NO:2. As such, the Examiner alleges that the claims embrace polynucleotides having broadly divergent properties which are not adequately described in terms of structure and function.

Applicants respectfully traverse and submit that the Examiner's interpretation of the claims is not reasonable in light of the disclosure in the specification or the claims viewed as a whole. In order to advance the prosecution of the present application, however, the claims have been amended in accordance with the Examiner's suggestion. In particular, the claims have been amended to include the definite article "the" in refering to a sequence identified by a SEQ ID NO. For example, claim 5 has been amended to recite "having the amino acid sequence as set forth in SEQ ID NO:2"; claim 7 has been amended to recite "having the amino acid sequence as set forth in SEQ ID NO:2" and "having the nucleotide sequence as set forth in SEQ ID NO:1"; claim 10 has been amended to recite "having the nucleic acid sequence set forth in SEQ ID NO:5"; and claim 26 has been amended to recite "having the nucleotide sequence as

set forth in SEQ ID NO:3". Additionally, claims 8, 9, 23 and 24 have been canceled herein and claim 11 has been amended to depend from claim 7.

As such, the current claims are more clearly directed to polynucleotides comprising the entire seqence set forth in the respective SEQ ID NOs recited in the claims. Accordingly, withdrawal of the rejection of claims 5, 7-15, and 23-26 under 35 U.S.C. 112, first paragraph, is respectfully requested.

Rejection Under 35 U.S.C. § 102(e)

The rejection of claim 26 under 35 U.S.C. § 102(e) as allegedly being anticipated by Schlegel et al. (WO 01/60860) is respectfully traversed.

It is alleged that Schlegel discloses a nucleic acid comprising a sequence that is identical to nucleotides 1-4727 of the instant SEQ ID NO:3 and encodes the instant SEQ ID NO:4 (see also, Office communication mailed 4/28/2004). Applicants again point out, however, that according to the sequence alignment provided by the Examiner, the nucleic acid sequence of Schlegel contains bases that do not match SEQ ID NO:3 and that Schlegel does not disclose a complete sequence as set forth in SEQ ID NO:3. The Examiner's attention is respectfully drawn to page 5, second column of the sequence alignment provided by the Examiner in the Office communication mailed 4/28/2004, which illustrates mismatched bases at bases 1963 and 2071 of the query sequence (a copy of the sequence alignment marked to show the mismatched bases is submitted herein as Exhibit A). As such, Schlegel does not teach a polynucleotide having the nucleotide sequence as set forth in SEQ ID NO:3, as currently claimed.

It is further alleged in the Office action that the claim is not limited to a polynucleotide comprising the entire SEQ ID NO:3, but encompasses a polynucleotide comprising any portion of SEQ ID NO:3. As set forth above, however, claim 26 has been amended to recite "a polynucleotide having the nucleotide sequence as set forth in SEQ ID NO:3" and, therefore, is more clearly drawn to a polynucleotide comprising the full length SEQ ID NO:3.

The Examiner further alleges that the fragments of SEQ ID NO:3 encompased by the claims are fully disclosed by Schlegel. Applicants point out, however, that while Schlegel

appears to teach a 4804 base nucleic acid sequence that is not identical to the current SEQ ID NO:3, Schlegel fails to teach polynucleotides limited to any particular segment of the prior art polynucleotide. More specifically, Schlegel does not teach a polynucleotide consisting of a polynucleotide as set forth in nucleic acid residues 1-331, 799-903, 1232-1543, 2147-2486, or 2964-4756 of SEQ ID NO:3, as required by the current claim 26. Applicants submit that these elements are missing from the teachings of Schlegel, thereby precluding a finding of anticipation.

It is further noted in the Office action that the rejection has not been set forth against claims directed to a polynucleotide encoding a polypeptide as set forth in SEQ ID NO:4 because the Examiner was unable to determine if such a polynucleotide was taught in the priority documents of Schlegel. A review of the priority documents of Schlegel by the Applicants similarly did not reveal any teachings as to a polynucleotide encoding a polypeptide as set forth in SEQ ID NO:4, as currently claimed. If the Examiner believes this to be in error, Applicants invite the Examiner to specifically point out where in the priority documents of Schlegel the claimed polynucleotide can be found. Applicants submit that the filing date of the current application and the support for the claimed invention is prior to the filing date of Schlegel.

In summary, for the reasons set forth above, it is submitted that the cited reference does not teach each and every element of the claimed invention. Accordingly, removal of the rejection of claim 26 under 35 U.S.C. § 102(e), as allegedly lacking novelty in light of Schlegel et al., is respectfully requested.

In view of the above amendments and remarks, Applicants believe that all claims are now in condition for allowance, which action is respectfully requested. The Examiner is invited to contact Applicants' undersigned representative if there are any questions relating to this application.

Please charge any additional fees, or make any credits, to Deposit Account No. 07-1896.

Respectfully submitted,

Date: April 15, 2005

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Facsimile: (858) 677-1465

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4365 Executive Drive, Suite 1100
San Diego, CA 92121-2133
USPTO CUSTOMER NO. 28213

Attachment: Exhibit A

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Qy      3721 CAGCCAAAGCACTGCAGAAGAATGCCAGTCGCCCTATGGTTATTCAGGAATCAAAGTCTT 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 CAGCCAAAGCACTGCAGAAGAATGCCAGTCGCCCTATGGTTATTCAGGAATCAAAGTCTT 3780

Qy      3781 TGCTCAGAAATCCTTTTGAAGCCATCAGACCAGGAAGTGCTCAACAGGTGAAGACAGGCT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 TGCTCAGAAATCCTTTTGAAGCCATCAGACCAGGAAGTGCTCAACAGGTGAAGACAGGCT 3840

Qy      3841 CACTGCTAAACCAGCCCAAAGCTGTGCTTCAGAAACTGGCTGCTCTCTCTGACCATAACC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 CACTGCTAAACCAGCCCAAAGCTGTGCTTCAGAAACTGGCTGCTCTCTCTGACCATAACC 3900

Qy      3901 CCAGTGCTCCTCGAAATTCAAGAAACTTTGTCTTTCATACACTTTCTCCTGTCAAGGCTG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 CCAGTGCTCCTCGAAATTCAAGAAACTTTGTCTTTCATACACTTTCTCCTGTCAAGGCTG 3960

Qy      3961 AGGCGGCAAAGGAATCGTCTAAGTCTCAGAAGATCCCAGAGAAGGACTCTGACTGGCTCA 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 AGGCGGCAAAGGAATCGTCTAAGTCTCAGAAGATCCCAGAGAAGGACTCTGACTGGCTCA 4020

Qy      4021 CCTGGAGTGGAGCTCCTATCCCTGGATTCTTCAGGCTTTCATTTGACCCACATGGTTAAG 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 CCTGGAGTGGAGCTCCTATCCCTGGATTCTTCAGGCTTTCATTTGACCCACATGGTTAAG 4080

Qy      4081 CTGGGAGAGACAGAGTCCAAAGAGAGGCGGAGAAGGGCTATTCTGGGCAGAACAAACAAT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 CTGGGAGAGACAGAGTCCAAAGAGAGGCGGAGAAGGGCTATTCTGGGCAGAACAAACAAT 4140

Qy      4141 TGATGACTTTATGGCTCTGTGGTCTGGGCAGAACTGCATAACCCTAGATCACCAAAGCTG 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 TGATGACTTTATGGCTCTGTGGTCTGGGCAGAACTGCATAACCCTAGATCACCAAAGCTG 4200

Qy      4201 AGAGCCTTTAGGAGTGAGGATTTGGGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 AGAGCCTTTAGGAGTGAGGATTTGGGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCA 4260

Qy      4261 CTTTGGGAGGCCGAGGTGGGTGGATCACAAGGTCAGGAGATCAAGACCAACCTGACCAAC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CTTTGGGAGGCCGAGGTGGGTGGATCACAAGGTCAGGAGATCAAGACCAACCTGACCAAC 4320

Qy      4321 ATGGTGAGGCCCCATCTCTACTAAAAATACAAAAATTAGCTGACGTGATGCATGCACCTG 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 ATGGTGAGGCCCCATCTCTACTAAAAATACAAAAATTAGCTGACGTGATGCATGCACCTG 4380

Qy      4381 TAATCCCAGCTACTCGGGAGGCTGAGGCGGGAGAATCGCTTGAACCCGGGAGGTTGGAGG 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 TAATCCCAGCTACTCGGGAGGCTGAGGCGGGAGAATCGCTTGAACCCGGGAGGTTGGAGG 4440

Qy      4441 TTGCGGTGGGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGGGACTCCAT 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 TTGCGGTGGGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGGGACTCCAT 4500

Qy      4501 CTCAAAAAAAAAAAAAAAAAAGTGAGGATTTGGGTCACCCCAGGCTGAAGGCCAGGGGAA 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 CTCAAAAAAAAAAAAAAAAAAGTGAGGATTTGGGTCACCCCAGGCTGAAGGCCAGGGGAA 4560

Qy      4561 CCTGAATGATAAGGGAAGGGAAAACTTAGGCCACAGTCTGATTAGAAATGGGGCTGAATT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CCTGAATGATAAGGGAAGGGAAAACTTAGGCCACAGTCTGATTAGAAATGGGGCTGAATT 4620

Qy      4621 CCACCCTGTTTTTCCTTTACTGGAGATTCAATTTGAATTACTCTGCCTCCCTTCTTATTC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CCACCCTGTTTTTCCTTTACTGGAGATTCAATTTGAATTACTCTGCCTCCCTTCTTATTC 4680

Qy      4681 CTTTTCCCTTTTAAAATAGTCATCATAATCATAAAAATTTCTTTTCCAAAAAAAAAAAAA 4740
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CTTTTCCCTTTTAAAA-AGTCATCATAATCATAAAAATTTCTTTTCCAAAAAAAAAAAAA 4739

Qy      4741 AAAAAAAAAAAAAAAA 4756
             ||||||||||||||||
Db      4740 AAAAAAAAAAAAAAAA 4755
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RESULT 2
ABV30199
ID ABV30199 standard; cDNA; 4804 BP.
XX
AC ABV30199;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 30190.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 6542-6543; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ Sequence 4804 BP; 1605 A; 910 C; 1244 G; 1016 T; 29 other;

Query Match 99.3%; Score 4723.8; DB 23; Length 4804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4725; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GACGGCGGCAGCCGCTGCTCTCCGGCTGAGGGAATCAGAGACAGCTCCGTCCCTAGTGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GACGGCGGGAGCCGCTGCTCTCCGGCTGAGGGAATCAGAGACAGCTCCGTCCCTAGTGGA 108

Qy         61 GCGCAGGGGAGGCAGAAGTCATGACAGGCGAGGTGGGTTCTGAGGTTCACCTAGAAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GCGCAGGGGAGGCAGAAGTCATGACAGGCGAGGTGGGTTCTGAGGTTCACCTAGAAATCA 168

Qy        121 ATGACCCAAACGTCATTTCACAAGAGGAAGCAGATAGTCCTTCAGATAGTGGACAGGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        169 ATGACCCAAACGTCATTTCACAAGAGGAAGCAGATAGTCCTTCAGATAGTGGACAGGGCA 228
Qy        181 GCTATGAAACAATTGGACCCTTGAGTGAAGGAGATTCAGATGAAGAGATATTTGTAAGTA 240
Db        229 GCTATGAAACAATTGGACCCTTGAGTGAAGGAGATTCAGATGAAGAGATATTTGTAAGTA 288
Qy        241 AGAAGTTGAAAAACAGGAAGGTTCTACAAGACAGTGATTCCGAAACAGAGGACACAAATG 300
Db        289 AGAAGTTGAAAAACAGGAAGGTTCTACAAGACAGTGATTCCGAAACAGAGGACACAAATG 348
Qy        301 CCTCTCCAGAGAAAACTACCTATGACAGTGCCGAGGAGGAAAATAAAGAGAATTTATATG 360
Db        349 CCTCTCCAGAGAAAACTACCTATGACAGTGCCGAGGAGGAAAATAAAGAGAATTTATATG 408
Qy        361 CTGGGAAAAATACAAAAATCAAAAGGATTTACAAAACTGTGGCAGACAGTGATGAAAGTT 420
Db        409 CTGGGAAAAATACAAAAATCAAAAGGATTTACAAAACTGTGGCAGACAGTGATGAAAGTT 468
Qy        421 ACATGGAAAAGTCTTTGTATCAGGAAAATCTTGAAGCGCAAGTGAAACCTTGCTTAGAGC 480
Db        469 ACATGGAAAAGTCTTTGTATCAGGAAAATCTTGAAGCGCAAGTGAAACCTTGCTTAGAGC 528
Qy        481 TGAGTCTTCAGTCTGGAAACTCTACAGACTTTACCACTGACAGAAAGAGTTCCAAAAAGC 540
Db        529 TGAGTCTTCAGTCTGGAAACTCTACAGACTTTACCACTGACAGAAAGAGTTCCAAAAAGC 588
Qy        541 ACATACATGATAAAGAAGGAACTGCAGGAAAAGCAAAAGTAAAATCAAAAAGAAGACTTG 600
Db        589 ACATACATGATAAAGAAGGAACTGCAGGAAAAGCAAAAGTAAAATCAAAAAGAAGACTTG 648
Qy        601 AGAAAGAGGAGAGAAAAATGGAAAAAATTAGACAGCTAAAAAAGAAGGAAACAAAAAACC 660
Db        649 AGAAAGAGGAGAGAAAAATGGAAAAAATTAGACAGCTAAAAAAGAAGGAAACAAAAAACC 708
Qy        661 AGGAAGATGATGTAGAACAGCCATTTAATGACAGTGGCTGTCTTCTTGTGGATAAAGACC 720
Db        709 AGGAAGATGATGTAGAACAGCCATTTAATGACAGTGGCTGTCTTCTTGTGGATAAAGACC 768
Qy        721 TTTTTGAAACTGGGTTGGAGGATGAAAATAACTCTCCATTGGAAGATGAAGAGTCATTAG 780
Db        769 TTTTTGAAACTGGGTTGGAGGATGAAAATAACTCTCCATTGGAAGATGAAGAGTCATTAG 828
Qy        781 AATCAATAAGAGCAGCTGTAAAAAACAAAGTAAAAAAGCACAAGAAAAAAGAACCATCTT 840
Db        829 AATCAATAAGAGCAGCTGTAAAAAACAAAGTAAAAAAGCACAAGAAAAAAGAACCATCTT 888
Qy        841 TGGAGAGTGGGGTCCATTCATTTGAGGAAGGAAGTGAGTTATCAAAAGGAACCACGAGGA 900
Db        889 TGGAGAGTGGGGTCCATTCATTTGAGGAAGGAAGTGAGTTATCAAAAGGAACCACGAGGA 948
Qy        901 AGGAAAGAAAGGCAGCCAGATTAAGTAAAGAAGCATTAAAACAACTGCATAGTGAGACTC 960
Db        949 AGGAAAGAAAGGCAGCCAGATTAAGTAAAGAAGCATTAAAACAACTGCATAGTGAGACTC 1008
Qy        961 AGCGCCTTATTCGAGAGTCTGCACTGAACCTTCCATATCATATGCCTGAGAATAAAACCA 1020
Db       1009 AGCGCCTTATTCGAGAGTCTGCACTGAACCTTCCATATCATATGCCTGAGAATAAAACCA 1068
Qy       1021 TTCATGATTTCTTCAAACGTAAACCCCGGCCCACTTGCCACGGAAATGCCATGGCACTAT 1080
Db       1069 TTCATGATTTCTTCAAACGTAAACCCCGGCCCACTTGCCACGGAAATGCCATGGCACTAT 1128
Qy       1081 TGAAGTCATCTAAATATCAGTCAAGCCATCACAAAGAAATCATAGACACTGCAAATACTA 1140
Db       1129 TGAAGTCATCTAAATATCAGTCAAGCCATCACAAAGAAATCATAGACACTGCAAATACTA 1188
Qy       1141 CTGAAATGAACAGTGATCACCATAGTAAAGGTTCTGAGCAGACAACAGGTGCAGAAAATG 1200
Db       1189 CTGAAATGAACAGTGATCACCATAGTAAAGGTTCTGAGCAGACAACAGGTGCAGAAAATG 1248
Qy       1201 AAGTGGAAACTAATGCACTCCCTGTAGTTTCAAAGGAAACCCAGATCATTACTGGATCAG 1260
Db       1249 AAGTGGAAACTAATGCACTCCCTGTAGTTTCAAAGGAAACCCAGATCATTACTGGATCAG 1308

Qy       1261 ATGAGTCTTGCAGGAAGGATTTGGTAAAAAATGAAGAGCTAGAAATTCAGGAGAAACAGA 1320
Db       1309 ATGAGTCTTGCAGGAAGGATTTGGTAAAAAATGAAGAGCTAGAAATTCAGGAGAAACAGA 1368
Qy       1321 AGCAGAGTGACATTAGACCTTCACCTGGGGACAGCTCAGTGTTGCAACAGGAATCCAACT 1380
Db       1369 AGCAGAGTGACATTAGACCTTCACCTGGGGACAGCTCAGTGTTGCAACAGGAATCCAACT 1428
Qy       1381 TCCTCGGGAACAATCACAGTGAGGAATGTCAGGTTGGAGGGCTTGTAGCATTTGAACCTC 1440
Db       1429 TCCTCGGGAACAATCACAGTGAGGAATGTCAGGTTGGAGGGCTTGTAGCATTTGAACCTC 1488
Qy       1441 ATGCCCTGGAGGGTGAAGGCCCCCAAAATCCAGAAGAAACAGATGAGAAAGTGGAAGAGC 1500
Db       1489 ATGCCCTGGAGGGTGAAGGCCCCCAAAATCCAGAAGAAACAGATGAGAAAGTGGAAGAGC 1548
Qy       1501 CTGAGCAGCAAAATAAATCATCAGCAGTTGGGCCACCTGAAAAAGTGAGACGGTTTACTC 1560
Db       1549 CTGAGCAGCAAAATAAATCATCAGCAGTTGGGCCACCTGAAAAAGTGAGACGGTTTACTC 1608
Qy       1561 TGGATAGACTTAAGCAACTGGGAGTAGATGTTTCCATTAAACCACGGCTAGGTGCTGATG 1620
Db       1609 TGGATAGACTTAAGCAACTGGGAGTAGATGTTTCCATTAAACCACGGCTAGGTGCTGATG 1668
Qy       1621 AAGATTCCTTTGTGATACTTGAACCTGAAACCAACAGAGAACTGGAAGCCTTGAAGCAGC 1680
Db       1669 AAGATTCCTTTGTGATACTTGAACCTGAAACCAACAGAGAACTGGAAGCCTTGAAGCAGC 1728
Qy       1681 GTTTCTGGAAGCATGCTAATCCAGCAGCCAAACCCAGGGCTGGTCAGACAGTGAATGTGA 1740
Db       1729 GTTTCTGGAAGCATGCTAATCCAGCAGCCAAACCCAGGGCTGGTCAGACAGTGAATGTGA 1788
Qy       1741 ACGTCATAGTGAAAGACATGGGCACTGATGGAAAGGAAGAGCTAAAAGCAGATGTGGTAC 1800
Db       1789 ACGTCATAGTGAAAGACATGGGCACTGATGGAAAGGAAGAGCTAAAAGCAGATGTGGTAC 1848
Qy       1801 CTGTGACTTTAGCACCTAAGAAGTTGGATGGAGCAAGCCACACAAAACCAGGTGAAAAGC 1860
Db       1849 CTGTGACTTTAGCACCTAAGAAGTTGGATGGAGCAAGCCACACAAAACCAGGTGAAAAGC 1908
Qy       1861 TTCAGGTGTTAAAAGCTAAACTGCAAGAAGCAATGAAACTCCGAAGGTTTGAGGAGCGCC 1920
Db       1909 TTCAGGTGTTAAAAGCTAAACTGCAAGAAGCAATGAAACTCCGAAGGTTTGAGGAGCGCC 1968
Qy       1921 AGAAGCGCCAAGCACTGTTTAAATTAGATAATGAAGATGGGTCTGAGGAAGAGGAGGAGG 1980
Db       1969 AGAAGCGCCAAGCACTGTTTAAATTAGATAATGAAGATGGGTCTGAGGAAGAGGAGGAGG 2028
Qy       1981 AAGAGGAAGAAATGACAGATGAGTCTGAGGAAGATGGAGAAGAGAAGGTAGAGAAAGAAG 2040
Db       2029 AAGAGGAAGAAATGACAGATGAGTCTGAGGAAGATGGAGAAGAGAAGGTAGAGAAAGAAG 2088
Qy       2041 AGAAAGAGGAAGAACTAGAGGAAGAGGAGGGGAAAGAAGAGGAGGAGGAAGAAGAAGGAA 2100
Db       2089 AGAAAGAGGAAGAACTAGAGGAAGAGGAGGAGAAAGAAGAGGAGGAGGAAGAAGAAGGAA 2148
Qy       2101 ATCAGGAGACTGCAGAATTCCTTCTTAGTAGTGAAGAAATAGAAACAAAAGATGAAAAAG 2160
Db       2149 ATCAGGAGACTGCAGAATTCCTTCTTAGTAGTGAAGAAATAGAAACAAAAGATGAAAAAG 2208
Qy       2161 AAATGGATAAAGAAAATAATGATGGCAGTAGTGAAATTGGCAAGGCAGTTGGCTTCCTCT 2220
Db       2209 AAATGGATAAAGAAAATAATGATGGCAGTAGTGAAATTGGCAAGGCAGTTGGCTTCCTCT 2268
Qy       2221 CTGTTCCCAAGTCTCTCTCATCAGATTCTACTTTACTTCTGTTTAAGGACAGCTCTTCCA 2280
Db       2269 CTGTTCCCAAGTCTCTCTCATCAGATTCTACTTTACTTCTGTTTAAGGACAGCTCTTCCA 2328
Qy       2281 AGATGGGTTACTCTCCTACTGAAGAAAAATCAGAAACAGATGAAAACTCAGGCAAGCAGC 2340
Db       2329 AGATGGGTTACTCTCCTACTGAAGAAAAATCAGAAACAGATGAAAACTCAGGCAAGCAGC 2388
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Qy    2341 CTAGCAAACTGGATGAGGATGATTCATGTTCATTGCTAACAAAGGAGAGCAGCCACAATA 2400
Db    2389 CTAGCAAACTGGATGAGGATGATTCATGTTCATTGCTAACAAAGGAGAGCAGCCACAATA 2448
Qy    2401 GCAGCTTTGAGCTGATTGGCTCCACGATTCCATCCTATCAGCCTTGCAACAGACAAACAG 2460
Db    2449 GCAGCTTTGAGCTGATTGGCTCCACGATTCCATCCTATCAGCCTTGCAACAGACAAACAG 2508
Qy    2461 GCCGTGGGACCAGTTTTTTCCCTACAGCAGGAGGATTCAGATCTCCTTCCCCTGGGCTAT 2520
Db    2509 GCCGTGGGACCAGTTTTTTCCCTACAGCAGGAGGATTCAGATCTCCTTCCCCTGGGCTAT 2568
Qy    2521 TTCGAGCCAGTTTGGTCAGCTCAGCTTCTAAGAGTTCAGGGAAACTGTCTGAGCCTTCAC 2580
Db    2569 TTCGAGCCAGTTTGGTCAGCTCAGCTTCTAAGAGTTCAGGGAAACTGTCTGAGCCTTCAC 2628
Qy    2581 TTCCCATAGAGGATTCCCAGGATCTGTATAACGCCTCCCCAGAGCCTAAGACACTTTTCC 2640
Db    2629 TTCCCATAGAGGATTCCCAGGATCTGTATAACGCCTCCCCAGAGCCTAAGACACTTTTCC 2688
      2641 TAGGAGCAGGAGACTTCCAGTTCTGTTTAGAAGATGACACTCAGAGCCAACTGTTGGATG 2700
Db    2689 TAGGAGCAGGAGACTTCCAGTTCTGTTTAGAAGATGACACTCAGAGCCAACTGTTGGATG 2748
Qy    2701 CAGATGGGTTCTTAAATGTTAGAAACCACAGGAATCAGTACCAAGCTTTGAAGCCTCGAT 2760
Db    2749 CAGATGGGTTCTTAAATGTTAGAAACCACAGGAATCAGTACCAAGCTTTGAAGCCTCGAT 2808
Qy    2761 TGCCATTGGCCAGTATGGATGAGAATGCCATGGATGCCAACATGGATGAGCTGTTGGATT 2820
Db    2809 TGCCATTGGCCAGTATGGATGAGAATGCCATGGATGCCAACATGGATGAGCTGTTGGATT 2868
Qy    2821 TGTGTACTGGAAAGTTCACATCTCAGGCTGAAAAACATCTACCCAGGAAGAGTGACAAGA 2880
Db    2869 TGTGTACTGGAAAGTTCACATCTCAGGCTGAAAAACATCTACCCAGGAAGAGTGACAAGA 2928
Qy    2881 AAGAGAACATGGAGGAACTTCTGAACCTTTGTTCAGGAAAATTCACTTCTCAGGATGCCT 2940
Db    2929 AAGAGAACATGGAGGAACTTCTGAACCTTTGTTCAGGAAAATTCACTTCTCAGGATGCCT 2988
Qy    2941 CCACTCCAGCCTCATCAGAGTTAAATAAACAGGAGAAGGAGAGCAGCATGGGTGATCCAA 3000
Db    2989 CCACTCCAGCCTCATCAGAGTTAAATAAACAGGAGAAGGAGAGCAGCATGGGTGATCCAA 3048
Qy    3001 TGGAAGAAGCACTTGCTCTTTGCTCAGGCTCTTTTCCCACAGACAAGGAAGAGGAAGACG 3060
Db    3049 TGGAAGAAGCACTTGCTCTTTGCTCAGGCTCTTTTCCCACAGACAAGGAAGAGGAAGACG 3108
      3061 AGGAGGAGGAATTTGGAGACTTTCGGCTTGTTTCAAATGATAATGAGTTTGATAGTGATG 3120
Db    3109 AGGAGGAGGAATTTGGAGACTTTCGGCTTGTTTCAAATGATAATGAGTTTGATAGTGATG 3168
Qy    3121 AGGATGAACACAGTGACTCTGGTAATGATCTGGCACTGGAAGACCATGAAGATGATGATG 3180
Db    3169 AGGATGAACACAGTGACTCTGGTAATGATCTGGCACTGGAAGACCATGAAGATGATGATG 3228
Qy    3181 AAGAAGAACTCCTGAAGCGATCTGAGAAGTTGAAAAGGCAAATGAGGTTGAGGAAATACC 3240
Db    3229 AAGAAGAACTCCTGAAGCGATCTGAGAAGTTGAAAAGGCAAATGAGGTTGAGGAAATACC 3288
Qy    3241 TGGAGGATGAGGCAGAGGTGTCAGGAAGTGATGTGGGAAGCGAAGATGAGTATGATGGGG 3300
Db    3289 TGGAGGATGAGGCAGAGGTGTCAGGAAGTGATGTGGGAAGCGAAGATGAGTATGATGGGG 3348
Qy    3301 AAGAAATTGATGAATATGAAGAGGACGTAATTGATGAAGTACTTCCTTCTGATGAGGAAC 3360
Db    3349 AAGAAATTGATGAATATGAAGAGGACGTAATTGATGAAGTACTTCCTTCTGATGAGGAAC 3408
Qy    3361 TGCAGAGTCAAATCAAGAAAATACACATGAAAACTATGTTGGATGATGATAAGCGACAGC 3420
Db    3409 TGCAGAGTCAAATCAAGAAAATACACATGAAAACTATGTTGGATGATGATAAGCGACAGC 3468
Qy    3421 TACGTTTATACCAAGAGAGGTACCTTGCTGATGGGGATCTGCACAGCGATGGTCCTGGGC 3480
Db    3469 TACGTTTATACCAAGAGAGGTACCTTGCTGATGGGGATCTGCACAGCGATGGTCCTGGGC 3528
Qy    3481 GAATGAGGAAGTTTCGATGGAAAAACATAGATGATGCTTCCCAGATGGACTTGTTCCACA 3540
Db    3529 GAATGAGGAAGTTTCGATGGAAAAACATAGATGATGCTTCCCAGATGGACTTGTTCCACA 3588
Qy    3541 GAGACTCTGATGATGATCAGACTGAAGAACAGCTTGATGAGTCAGAAGCCAGGTGGAGGA 3600
Db    3589 GAGACTCTGATGATGATCAGACTGAAGAACAGCTTGATGAGTCAGAAGCCAGGTGGAGGA 3648
Qy    3601 AGGAGCGAATTGAACGAGAGCAGTGGCTTCGGGACATGGCACAGCAGGGGAAAATTACAG 3660
Db    3649 AGGAGCGAATTGAACGAGAGCAGTGGCTTCGGGACATGGCACAGCAGGGGAAAATTACAG 3708
Qy    3661 CTGAAGAAGAAGAAGAAATTGGGGAGGACAGTCAGTTTATGATACTGGCCAAGAAAGTTA 3720
Db    3709 CTGAAGAAGAAGAAGAAATTGGGGAGGACAGTCAGTTTATGATACTGGCCAAGAAAGTTA 3768
Qy    3721 CAGCCAAAGCACTGCAGAAGAATGCCAGTCGCCCTATGGTTATTCAGGAATCAAAGTCTT 3780
Db    3769 CAGCCAAAGCACTGCAGAAGAATGCCAGTCGCCCTATGGTTATTCAGGAATCAAAGTCTT 3828
Qy    3781 TGCTCAGAAATCCTTTTGAAGCCATCAGACCAGGAAGTGCTCAACAGGTGAAGACAGGCT 3840
Db    3829 TGCTCAGAAATCCTTTTGAAGCCATCAGACCAGGAAGTGCTCAACAGGTGAAGACAGGCT 3888
Qy    3841 CACTGCTAAACCAGCCCAAAGCTGTGCTTCAGAAACTGGCTGCTCTCTCTGACCATAACC 3900
Db    3889 CACTGCTAAACCAGCCCAAAGCTGTGCTTCAGAAACTGGCTGCTCTCTCTGACCATAACC 3948
Qy    3901 CCAGTGCTCCTCGAAATTCAAGAAACTTTGTCTTTCATACACTTTCTCCTGTCAAGGCTG 3960
Db    3949 CCAGTGCTCCTCGAAATTCAAGAAACTTTGTCTTTCATACACTTTCTCCTGTCAAGGCTG 4008
Qy    3961 AGGCGGCAAAGGAATCGTCTAAGTCTCAGAAGATCCCAGAGAAGGACTCTGACTGGCTCA 4020
Db    4009 AGGCGGCAAAGGAATCGTCTAAGTCTCAGAAGATCCCAGAGAAGGACTCTGACTGGCTCA 4068
Qy    4021 CCTGGAGTGGAGCTCCTATCCCTGGATTCTTCAGGCTTTCATTTGACCCACATGGTTAAG 4080
Db    4069 CCTGGAGTGGAGCTCCTATCCCTGGATTCTTCAGGCTTTCATTTGACCCACATGGTTAAG 4128
Qy    4081 CTGGGAGAGACAGAGTCCAAAGAGAGGCGGAGAAGGGCTATTCTGGGCAGAACAAACAAT 4140
Db    4129 CTGGGAGAGACAGAGTCCAAAGAGAGGCGGAGAAGGGCTATTCTGGGCAGAACAAACAAT 4188
Qy    4141 TGATGACTTTATGGCTCTGTGGTCTGGGCAGAACTGCATAACCCTAGATCACCAAAGCTG 4200
Db    4189 TGATGACTTTATGGCTCTGTGGTCTGGGCAGAACTGCATAACCCTAGATCACCAAAGCTG 4248
Qy    4201 AGAGCCTTTAGGAGTGAGGATTTGGGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCA 4260
Db    4249 AGAGCCTTTAGGAGTGAGGATTTGGGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCA 4308
Qy    4261 CTTTGGGAGGCCGAGGTGGGTGGATCACAAGGTCAGGAGATCAAGACCAACCTGACCAAC 4320
Db    4309 CTTTGGGAGGCCGAGGTGGGTGGATCACAAGGTCAGGAGATCAAGACCAACCTGACCAAC 4368
Qy    4321 ATGGTGAGGCCCCATCTCTACTAAAAATACAAAAATTAGCTGACGTGATGCATGCACCTG 4380
Db    4369 ATGGTGAGGCCCCATCTCTACTAAAAATACAAAAATTAGCTGACGTGATGCATGCACCTG 4428
Qy    4381 TAATCCCAGCTACTCGGGAGGCTGAGGCGGGAGAATCGCTTGAACCCGGGAGGTTGGAGG 4440
Db    4429 TAATCCCAGCTACTCGGGAGGCTGAGGCGGGAGAATCGCTTGAACCCGGGAGGTTGGAGG 4488
Qy    4441 TTGCGGTGGGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGGGACTCCAT 4500
Db    4489 TTGCGGTGGGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAGCGGGACTCCAT 4548
Qy    4501 CTCAAAAAAAAAAAAAAAAAAAGTGAGGATTTGGGTCACCCCAGGCTGAAGGCCAGGGGAA 4560
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Db       4549 CTCAAAAAAAAAAAAAAAAAAGTGAGGATTTGGGTCACCCCAGGCTGAAGGCCAGGGGAA 4608

Qy       4561 CCTGAATGATAAGGGAAGGGAAAACTTAGGCCACAGTCTGATTAGAAATGGGGCTGAATT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4609 CCTGAATGATAAGGGAAGGGAAAACTTAGGCCACAGTCTGATTAGAAATGGGGCTGAATT 4668

Qy       4621 CCACCCTGTTTTTCCTTTACTGGAGATTCAATTTGAATTACTCTGCCTCCCTTCTTATTC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4669 CCACCCTGTTTTTCCTTTACTGGAGATTCAATTTGAATTACTCTGCCTCCCTTCTTATTC 4728

Qy       4681 CTTTTCCCTTTTAAAATAGTCATCATAATCATAAAAATTTCTTTTCC 4727
             |||||||||||||||||||||||||||||||||||||||||||||||
Db       4729 CTTTTCCCTTTTAAAATAGTCATCATAATCATAAAAATTTCTTTTCC 4775
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RESULT 3
ABK52610
ID ABK52610 standard; DNA; 4754 BP.
XX
AC ABK52610;
XX
DT 27-AUG-2002 (first entry)
XX
DE DNA encoding Xenopus Claspin protein.
XX
KW ChK1 protein; SQ/TQ motif; isoelectric point; cell cycle progression;
KW nuclear localisation signal; DNA replication checkpoint; benign neoplasm;
KW cell proliferative disorder; malignant neoplasm; frog; claspin; gene; ds.
XX
OS Xenopus sp.
XX
FH Key Location/Qualifiers
FT CDS 71..3928
FT /*tag= a
FT /product= "Xenopus Claspin protein"
XX
PN WO200233115-A2.
XX
PD 25-APR-2002.
XX
PF 17-OCT-2001; 2001WO-US32316.
XX
PR 17-OCT-2000; 2000US-241246P.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Kumagai A, Dunphy WG;
XX
DR WPI; 2002-452394/48.
DR P-PSDB; AAU97586.
XX
PT Novel Claspin polypeptide specifically interacting with ChK1 protein
PT useful for identifying compound that modulates cell cycle progression
PT and for treating cell proliferative disorder like neoplasm -
XX
PS Claim 7; Fig 1; 97pp; English.
XX
CC The present invention relates to a new substantially pure Claspin
CC polypeptide that specifically interacts with a ChK1 protein, having SQ/TQ
CC motifs, an isoelectric point of 4.5 and at least one nuclear localisation
CC signal. The method of the invention is useful for identifying a compound
CC that modulates cell cycle progression and for modulating cell cycle
CC progression in a cell. The invention is useful for the proper operation
CC of DNA replication checkpoint in the cell cycle. The method is also
CC useful for treating a disorder associated with cell cycle progression
CC e.g. cell proliferative disorder such as benign or malignant neoplasm.
CC The molecules of the invention are also useful for detecting the altered
CC levels of claspin expression. The present nucleic acid sequence encodes
CC the Xenopus Claspin protein of the invention.
XX
SQ Sequence 4754 BP; 1658 A; 832 C; 1066 G; 1198 T; 0 other;

Query Match 15.4%; Score 730.2; DB 24; Length 4754;

Best Local Similarity 54.3%; Pred. No. 3e-111;
Matches 2085; Conservative 0; Mismatches 1523; Indels 231; Gaps 21;

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Qy        184 ATGAAACAATTGGACCCTTGAGTGAAGGAGATTCAGATGAAGAGATATTTGTAAGTAAGA 243
              || ||  | | ||     ||   ||   |||| ||||||| || || || ||  |||| |
Db        186 ATAAATTATTGGGTTGTGTGGAGGATAAAGATACAGATGATGAAATCTTGGTTCGTAAAA 245

Qy        244 AGTTGAAAAACAGGAAGGTTCTACAAGACAGTGA---TTCCGAAACAGAGGACACAAATG 300
              | |  ||||| | | | ||  |    || ||||   |  ||||  |  |||  |    |
Db        246 AATCTAAAAAGAAGGAAGTATTGGTGGATAGTGACAGTGACGAAGAATTGGAAATGCGTA 305

Qy        301 CCTCTCCAGAGAAAACTACCTATGACAGTGCCGAGGAGGAAAATAAAGAGAATTTATATG 360
              | | |||| ||    |      ||  ||   | ||||| ||| | |||| | | ||
Db        306 ATTTTGCAGATAATGTAAAGGGGCACTCTGATAATGAGGAGAATGAGGAGACTATGTCTG 365

Qy        361 CTGGGAAAAATACAAAAATCAAAAGGATTTACAAAACTGTGGCAGACAGTGATGAAAGTT 420
              ||   | | |.  ||||   | || |||      | ||||    ||||||||  | |||
Db        366 CTTATAGAGA---AAAACCAAGAAAGATCCGTTCAGCTGTATTGGACAGTGACAATAGTG 422

Qy        421 ACATGGAAAAGTCTTTGTATCAGGAAAATCTTGAAGCGCAAGTGAAACCTTGCTTAGAGC 480
              |    ||      | |  |       |    | ||   ||   ||
Db        423 ATCATGAGCTTGATGTTCAAATAAGTACAAGTCAAAATGCAGCTGAAATACCTGAGTCAG 482

Qy        481 TGAGTCTTCAGTCTGGAAACTCTACAGACTTTACCACTGACAGAAAGAGTTCCAAAAAGC 540
              |  |  |  |  ||   ||  |  |   |     | ||  ||          |
Db        483 AACATGATAGCTTGGAGAAGGAAACTCATACTGTGAAGCCTAAAACAAGCAAGTCCTTGA 542

Qy        541 ACATACATGATAAAGAAGGAACTGCAGGAAAAGCAAAAGTAAAATCAAAAAGAAGACTTG 600
              | | |||  | |       |  |  : ||  |  ||   ||||||||  | | | ||
Db        543 AAAAACAAACTGACACTAATAAAGAGGAAATCGTGAAGAATAAATCAAAGCGCAAAATTC 602

Qy        601 AGAAAGAGGAGAGAAAAATGGAAAAAATTAGACAGCTAAAAAAGAAGGAAACAAAAAACC 660
              |||||||  |||  |||| |   | ||      ||  ||||
Db        603 CGAAAGAGAAGATTAAAAGGAGGACAAAACAGAASTCAAAAGCA---------------- 646

Qy        661 AGGAAGATGATGTAGAACAGCCATTTAATGACAGTGGCTGTCTTCTTGTGGATAAAGACC 720
              |  | |||  |      |     ||  ||||||||||||||  | ||   |||  ||| |
Db        647 --GTTGCTGAAGCTAGGCCAAATTTAAATGACAGTGGCTGCTTACTCACAGATGGAGATC 704

Qy        721 TTTTTGAAACTGGGTTGGAGGATGAAAATAACTCTCCATTGGAAGATGAAGAGTCATTAG 780
              |||||||  | ||||  ||||  ||||  |    | |||      |||||  ||  ||  ||   | |
Db        705 TTTTTGACAATGGGGTGGAAAATGAGATGGATTCT---AATGAAGAAGAGGATTCTCTTG 761

Qy        781 AATCAATAAGAGCAGCTGTAAAAAACAAAGTAAAAAAAGCACAAGAAAAAAGAACCATCTT 840
              ||  | ||  | |||    | ||||  ||||  |            |||  |   |  |  ||
Db        762 AAGCTATCCGGGCAAAAATGAAAAGCAAACT-----------GAATAGTCATTCTGCTG 809

Qy        841 TGGAGAGTGGGGTCCATTCATTTGAGGAAGGAAGTGAGTTATCAAAAGGAACCACGAGGA 900
              |   ||  | |  |  | ||||    | | |  |   |  |    |  |  || |
Db        810 AAAATTTTGAAGACTTTGAACTTGATACTGAAGGCAATCAAGAATCCCCAGAAAAAAGAA 869

Qy        901 AGGAAAGAAAGGCAGCCAGATTAAGTAAAGAAGCATTAAAACAACTGCATAGTGAGACTC 960
              |||||  |||| || ||  || |  |||||||||  | ||||||  |||| |||||||| |
Db        870 AGGAACGAAAAGCTGCGCGACTTGGTAAAGAAGCCATGAAACAAATGCACAGTGAGACCC 929

Qy        961 AGCGCCTTATTCGAGAGTCTGCACTGAACCTTCCATATCATATGCCTGAGAATAAAACCA 1020
              |  | || || || || ||| |  |     | |||||||| | |||||    ||||| |
Db        930 AAAGACTAATACGTGAATCTTCTGTATCTTTACCATATCATCTACCTGAACCAAAAACAA 989

Qy       1021 TTCATGATTTCTTCAAACGTAAACCCCGGCCCACTTGCCACGGAAATGCCATGGCACTAT 1080
              | |||||||| |||||| |  , ||  ||||   ||| || |||||||| |||   ||
Db        990 TCCATGATTTTTTCAAAAGGCGTCCAAGGCCTCTTTGTCAAGGAAATGCAATGCAGCTTA 1049

Qy       1081 TGAAGTCATCTAAATATCAGTCAAGCCATCACAAAGAAATCATAGACACTGCAAATACTA 1140
              | |||||| | ||||| ||| |  ||  | |  |  |||  | |  || ||
Db       1050 TAAAGTCAACAAAATACCAGCCCTGCACTGAAGAGAAAAAAAAACCCAATG--------- 1100

Qy       1141 CTGAAATGAACAGTGATCACCATAGTAAAGGTTCTGAGCAGACAACAGGTGCAGAAAATG 1200
                                                  ||  ||  | ||||  |||  |
Db       1101 ----------------------------------------AGGAAATATGTGCTGAAGTTC 1121

Qy       1201 AAGTGGAAACTAATGCACTCCCTGTAGTTTCAAAGGAAACCCAGATCATTACTGGATCAG 1260
              || |     | |||        | || || | |    |  |         ||  |  |
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